OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/943,692

DATE: 09/21/2001
TIME: 18:02:38

Input Set : A:\Mobt195.ST25.txt
Output Set: N:\CRF3\09212001\I943692.raw

3 <110> APPLICANT: FISCHHOFF, DAVID A.
4 FUCHS, ROY L.
5 LAVRIK, PAUL B.
6 McPHERSON, SYLVIA A.
7 PERLAK, FREDERICK J.
9 <120> TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
11 <130> FILE REFERENCE: MOBT:195--1
M-> 13 <140> CURRENT APPLICATION NUMBER: US/09/943,692
C-> 13 <141> CURRENT FILING DATE: 2001-08-31
13 <150> PRIOR APPLICATION NUMBER: 09/027,998
14 <151> PRIOR FILING DATE: 1998-02-23
16 <160> NUMBER OF SEQ ID NOS: 54
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2615
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Chimeric toxin gene
29 <400> SEQUENCE: 1

ENTERED

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32 tgtataaatt atttatcttg aaaggaggga tgcctaaaaa cgaagaacat taaaaacata 120
34 tatttgcacc gtctaatgga tttatgaaaa atcattttat cagtttgaaa attatgtatt 180
36 atgataagaa agggaggaag aaaaatgaat ccgaacaatc gaagtgaaca tgatacaata 240
38 aaaactactg aaaataatga ggtgccaact aaccatgttc aatatccttt agcggaaact 300
40 ccaaatccaa cactagaaga tttaaattat aaagagtttt taagaatgac tgcagataat 360
42 aatacggaag cactagatag ctctacaaca aaagatgtca ttcaaaaagg catttccgta 420
44 gtaggtgatc tcctaggcgt agtaggtttc ccgtttggtg gagcgcttgt ttcgttttat 480
46 acaaactttt taaatactat ttggccaagt gaagacccgt ggaaggcttt tatggaacaa 540
48 gtagaagcat tgatggatca gaaaatagct gattatgcaa aaaataaagc tcttgcagag 600
50 ttacagggcc ttcaaaataa tgtcgaagat tatgtgagtg cattgagttc atggcaaaaa 660
52 aatcctgtga gttcacgaaa tccacatagc caggggcgga taagagagct gttttctcaa 720
54 gcagaaagtc attttcgtaa ttcaatgcct tcgtttgcaa tttctggata cgaggttcta 780
56 tttctaacaa catatgcaca agctgccaac acacatttat ttttactaaa agacgctcaa 840
58 atttatggag aagaatgggg atacgaaaaa gaagatattg ctgaatttta taaaagacaa 900
60 ctaaaactta cgcaagaata tactgaccat tgtgtcaaat ggtataatgt tggattagat 960
62 aaattaagag gttcatctta tgaatcttgg gtaaacttta accgttatcg cagagagatg 1020
64 acattaacag tattagattt aattgcacta tttccattgt atgatgttcg gctataccca 1080
66 aaagaagtta aaaccgaatt aacaagagac gttttaacag atccaattgt cggagtcaac 1140
68 aaccttaggg gctatggaac aaccttctct aatatagaaa attatattcg aaaaccacat 1200
70 ctatttgact atctgcatag aattcaattt cacacgcggt tccaaccagg atattatgga 1260
72 aatgactctt tcaattattg gtccggtaat tatgtttcaa ctagaccaag cataggatca 1320
74 aatgatataa tcacatctcc attctatgga aataaatcca gtgaacctgt acaaaattta 1380
76 gaatttaatg gagaaaaagt ctatagagcc gtagcaaata caaatcttgc ggtctggccg 1440
78 tccgctgtat attcaggtgt tacaaaagtg gaatttagcc aatataatga tcaaacagat 1500
80 gaagcaagta cacaaacgta cgactcaaaa agaaatgttg gcgcggtcag ctgggattct 1560
82 atcgatcaat tgcctccaga aacaacagat gaacctctag aaaagggata tagccatcaa 1620

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ctcaattatg taatgtgctt tttaatgcag ggtagtagag gaacaatccc agtgttaact 1680
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ccgttagtaa aggcatataa gttacaatct ggtgcttccg ttgtcgcagg tcctaggttt 1800
acaggaggag atatcattca atgcacagaa aatggaagtg cggcaactat ttacgttaca 1860
ccggatgtgt cgtactctca aaaatatcga gctagaattc attatgcttc tacatctcag 1920
ataacattta cactcagttt agacggggca ccatttaatc aatactattt cgataaaacg 1980
ataaataaag gagacacatt aacgtataat tcatttaatt tagcaagttt cagcacacca 2040
ttcgaattat cagggaataa cttacaaata ggcgtcacag gattaagtgc tggagataaa 2100
gtttatatag acaaaattga atttattcca gtgaattaaa ttaactagaa agtaaagaag 2160
tagtgaccat ctatgatagt aagcaaagga taaaaaaatg agttcataaa atgaataaca 2220
tagtgttctt caactttcgc tttttgaagg tagatgaaga acactatttt tattttcaaa 2280
atgaaggaag ttttaaatat gtaatcattt aaagggaaca atgaaagtag gaaataagtc 2340
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ttgtatacag agctgttgtt tccatcgagt tatgtcccat ttgattcgct aatagaacaa 2520
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tcttttcatc caaaagccaa gtgtatttct ctgta 2615

<210> SEQ ID NO: 2
<211> LENGTH: 644
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric toxin
<400> SEQUENCE: 2

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Thr Thr Glu
1 5 10 15
Asn Asn Glu Val Pro Thr Asn His Val Gln Tyr Pro Leu Ala Glu Thr
20 25 30
Pro Asn Pro Thr Leu Glu Asp Leu Asn Tyr Lys Glu Phe Leu Arg Met
35 40 45
Thr Ala Asp Asn Asn Thr Glu Ala Leu Asp Ser Ser Thr Thr Lys Asp
50 55 60
Val Ile Gln Lys Gly Ile Ser Val Val Gly Asp Leu Leu Gly Val Val
65 70 75 80
Gly Phe Pro Phe Gly Gly Ala Leu Val Ser Phe Tyr Thr Asn Phe Leu
85 90 95
Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Glu Gln
100 105 110
Val Glu Ala Leu Met Asp Gln Lys Ile Ala Asp Tyr Ala Lys Asn Lys
115 120 125
Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Val Glu Asp Tyr Val
130 135 140
Ser Ala Leu Ser Ser Trp Gln Lys Asn Pro Val Ser Ser Arg Asn Pro
145 150 155 160
His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
165 170 175
Phe Arg Asn Ser Met Pro Ser Phe Ala Ile Ser Gly Tyr Glu Val Leu
180 185 190
Phe Leu Thr Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Phe Leu Leu

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```
179         195                 200                 205
182 Lys Asp Ala Gln Ile Tyr Gly Glu Glu Trp Gly Tyr Glu Lys Glu Asp
183     210                 215                 220
186 Ile Ala Glu Phe Tyr Lys Arg Gln Leu Lys Leu Thr Gln Glu Tyr Thr
187 225                 230                 235                 240
190 Asp His Cys Val Lys Trp Tyr Asn Val Gly Leu Asp Lys Leu Arg Gly
191                 245                 250                 255
194 Ser Ser Tyr Glu Ser Trp Val Asn Phe Asn Arg Tyr Arg Arg Glu Met
195             260                 265                 270
198 Thr Leu Thr Val Leu Asp Leu Ile Ala Leu Phe Pro Leu Tyr Asp Val
199         275                 280                 285
202 Arg Leu Tyr Pro Lys Glu Val Lys Thr Glu Leu Thr Arg Asp Val Leu
203     290                 295                 300
206 Thr Asp Pro Ile Val Gly Val Asn Asn Leu Arg Gly Tyr Gly Thr Thr
207 305                 310                 315                 320
210 Phe Ser Asn Ile Glu Asn Tyr Ile Arg Lys Pro His Leu Phe Asp Tyr
211                 325                 330                 335
214 Leu His Arg Ile Gln Phe His Thr Arg Phe Gln Pro Gly Tyr Tyr Gly
215             340                 345                 350
218 Asn Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Ser Thr Arg Pro
219         355                 360                 365
222 Ser Ile Gly Ser Asn Asp Ile Ile Thr Ser Pro Phe Tyr Gly Asn Lys
223     370                 375                 380
226 Ser Ser Glu Pro Val Gln Asn Leu Glu Phe Asn Gly Glu Lys Val Tyr
227 385                 390                 395                 400
230 Arg Ala Val Ala Asn Thr Asn Leu Ala Val Trp Pro Ser Ala Val Tyr
231                 405                 410                 415
234 Ser Gly Val Thr Lys Val Glu Phe Ser Gln Tyr Asn Asp Gln Thr Asp
235             420                 425                 430
238 Glu Ala Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Val Gly Ala Val
239         435                 440                 445
242 Ser Trp Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp Glu Pro
243     450                 455                 460
246 Leu Glu Lys Gly Tyr Ser His Gln Leu Asn Tyr Val Met Cys Phe Leu
247 465                 470                 475                 480
250 Met Gln Gly Ser Arg Gly Thr Ile Pro Val Leu Thr Trp Thr His Lys
251                 485                 490                 495
254 Ser Val Asp Phe Phe Asn Met Ile Asp Ser Lys Lys Ile Thr Gln Leu
255             500                 505                 510
258 Pro Leu Val Lys Ala Tyr Lys Leu Gln Ser Gly Ala Ser Val Val Ala
259         515                 520                 525
262 Gly Pro Arg Phe Thr Gly Gly Asp Ile Ile Gln Cys Thr Glu Asn Gly
263     530                 535                 540
266 Ser Ala Ala Thr Ile Tyr Val Thr Pro Asp Val Ser Tyr Ser Gln Lys
267 545                 550                 555                 560
270 Tyr Arg Ala Arg Ile His Tyr Ala Ser Thr Ser Gln Ile Thr Phe Thr
271                 565                 570                 575
274 Leu Ser Leu Asp Gly Ala Pro Phe Asn Gln Tyr Tyr Phe Asp Lys Thr
275             580                 585                 590
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```
278 Ile Asn Lys Gly Asp Thr Leu Thr Tyr Asn Ser Phe Asn Leu Ala Ser
279         595                 600                 605
282 Phe Ser Thr Pro Phe Glu Leu Ser Gly Asn Asn Leu Gln Ile Gly Val
283     610                 615                 620
286 Thr Gly Leu Ser Ala Gly Asp Lys Val Tyr Ile Asp Lys Ile Glu Phe
287 625                 630                 635                 640
290 Ile Pro Val Asn
294 <210> SEQ ID NO: 3
295 <211> LENGTH: 15
296 <212> TYPE: PRT
297 <213> ORGANISM: Bacillus thuringiensis
W--> 298 <400> SEQUENCE: 3
300 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Thr Thr
301 1               5                   10                  15
304 <210> SEQ ID NO: 4
305 <211> LENGTH: 45
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Synthetic Oligonucleotide
312 <220> FEATURE:
313 <221> NAME/KEY: misc_feature
314 <222> LOCATION: (9)..(9)
315 <223> OTHER INFORMATION: N = A, C, G or T
319 <220> FEATURE:
320 <221> NAME/KEY: misc_feature
321 <222> LOCATION: (18)..(18)
322 <223> OTHER INFORMATION: N = A, C, G or T
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327 <221> NAME/KEY: misc_feature
328 <222> LOCATION: (21)..(21)
329 <223> OTHER INFORMATION: N = A, C, G or T
333 <220> FEATURE:
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335 <222> LOCATION: (33)..(33)
336 <223> OTHER INFORMATION: N = A, C, G or T
340 <220> FEATURE:
341 <221> NAME/KEY: misc_feature
342 <222> LOCATION: (42)..(42)
343 <223> OTHER INFORMATION: N = A, C, G or T
347 <220> FEATURE:
348 <221> NAME/KEY: misc_feature
349 <222> LOCATION: (45)..(45)
350 <223> OTHER INFORMATION: N = A, C, G or T
353 <400> SEQUENCE: 4
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357 <210> SEQ ID NO: 5
358 <211> LENGTH: 45
359 <212> TYPE: DNA
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Input Set : A:\Mobt195.ST25.txt
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360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: Synthetic Oligonucleotide
365 <220> FEATURE:
366 <221> NAME/KEY: misc_feature
367 <222> LOCATION: (9)..(9)
368 <223> OTHER INFORMATION: N = A, C, G or T
372 <220> FEATURE:
373 <221> NAME/KEY: misc_feature
374 <222> LOCATION: (33)..(33)
375 <223> OTHER INFORMATION: N = A, C, G or T
379 <220> FEATURE:
380 <221> NAME/KEY: misc_feature
381 <222> LOCATION: (42)..(42)
382 <223> OTHER INFORMATION: N = A, C, G or T
386 <220> FEATURE:
387 <221> NAME/KEY: misc_feature
388 <222> LOCATION: (45)..(45)
389 <223> OTHER INFORMATION: N = A, C, G or T
392 <400> SEQUENCE: 5
393 **atgaacccna acaacagaag tgagcacgac acnatcaaga cnacn** 45
396 <210> SEQ ID NO: 6
397 <211> LENGTH: 45
398 <212> TYPE: DNA
399 <213> ORGANISM: Artificial Sequence
401 <220> FEATURE:
402 <223> OTHER INFORMATION: Synthetic Oligonucleotide
404 <220> FEATURE:
405 <221> NAME/KEY: misc_feature
406 <222> LOCATION: (9)..(9)
407 <223> OTHER INFORMATION: N = A, C, G or T
411 <220> FEATURE:
412 <221> NAME/KEY: misc_feature
413 <222> LOCATION: (33)..(33)
414 <223> OTHER INFORMATION: N = A, C, G or T
418 <220> FEATURE:
419 <221> NAME/KEY: misc_feature
420 <222> LOCATION: (42)..(42)
421 <223> OTHER INFORMATION: N = A, C, G or T
425 <220> FEATURE:
426 <221> NAME/KEY: misc_feature
427 <222> LOCATION: (45)..(45)
428 <223> OTHER INFORMATION: N = A, C, G or T
431 <400> SEQUENCE: 6
432 **atgaatccna ataatcggtc cgaacatgat acnataaaaa cnacn** 45
435 <210> SEQ ID NO: 7
436 <211> LENGTH: 17
437 <212> TYPE: DNA
438 <213> ORGANISM: Artificial Sequence

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/943,692

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Input Set : A:\Mobt195.ST25.txt
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:298 M:283 W: Missing Blank Line separator, <400> field identifier
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1117 M:283 W: Missing Blank Line separator, <400> field identifier
L:1125 M:283 W: Missing Blank Line separator, <400> field identifier
L:1148 M:283 W: Missing Blank Line separator, <400> field identifier
L:1156 M:283 W: Missing Blank Line separator, <400> field identifier
L:1179 M:283 W: Missing Blank Line separator, <400> field identifier
L:1187 M:283 W: Missing Blank Line separator, <400> field identifier
L:1212 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:1215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54
L:1215 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:1218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54
L:1218 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2